

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 19, 2003, 15:02:10 ; Search time 72 seconds
(without alignments)
2713.136 Million cell updates/sec

Title: US-09-494-297-2
Perfect score: 3945
Sequence: 1 MKTRFNNKLTNTQRLVLS.....IAGISLGIWGHIRIRKHD 757

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues
Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database :
- 1: SPREMBL_23:*
 - 2: sp.archaea:*
 - 3: sp.bacteria:*
 - 4: sp.fungi:*
 - 5: sp.human:*
 - 6: sp.invertebrate:*
 - 7: sp.mammal:*
 - 8: sp.mhc:*
 - 9: sp.organelle:*
 - 10: sp.plant:*
 - 11: sp.podent:*
 - 12: sp.virus:*
 - 13: sp.vertebrate:*
 - 14: sp.unclassified:*
 - 15: sp.virus:*
 - 16: sp.bacteriap:*
 - 17: sp.archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	3941	99.9	2	08GRA2 streptococc
2	2058.5	52.2	2	08RP3 streptococc
3	1965.5	49.8	2	092B47 streptococc
4	1862	47.2	16	08K8U7 streptococc
5	1254.5	31.8	16	08P2W3 streptococc
6	633.5	16.1	2	054953 streptococc
7	633	16.0	2	08RP54 streptococc
8	611	15.5	2	033709 streptococc
9	603	15.3	2	001924 streptococc
10	523	13.3	2	047942 streptococc
11	272.5	6.9	2	033715 streptococc
12	262.5	6.7	104	2 033714 streptococc
13	241.5	6.1	108	2 033711 streptococc
14	236.5	6.0	340	16 09A1S2 streptococc
15	224.5	5.7	696	16 08P2V7 streptococc
16	223	5.7	733	2 08G9G1 streptococc

ALIGNMENTS

17	222.5	5.6	116	2	033721	033721 streptococc
18	211.5	5.4	92	2	033718	033718 streptococc
19	211.5	5.4	103	2	033712	033712 streptococc
20	210.5	5.3	102	2	033719	033719 streptococc
21	209.5	5.3	102	2	033716	033716 streptococc
22	205.5	5.2	93	2	033713	033713 streptococc
23	204.5	5.2	102	2	033720	033720 streptococc
24	202.5	5.1	93	2	033710	033710 streptococc
25	202.5	5.1	1368	16	093M90	093M90 clostridium
26	185	4.7	84	2	033717	033717 streptococc
27	180	4.6	597	2	P72416	P72416 streptococc
28	178	4.5	898	2	085081	085081 moraxella c
29	176	4.5	905	2	085088	085088 moraxella c
30	174.5	4.4	298	2	093ED6	093ED6 streptococc
31	167	4.2	344	16	08K8U5	08K8U5 streptococc
32	164	4.2	1039	2	P72534	P72534 streptococc
33	161	4.1	1160	2	08RM86	08RM86 streptococc
34	161	4.1	1386	16	092DL0	092DL0 listeria in
35	159	4.0	1243	2	048588	048588 lactococcus
36	159	4.0	1612	16	08T591	08T591 listeria mo
37	159	4.0	1681	5	08T1G8	08T1G8 dictyostell
38	158.5	4.0	3269	2	09RGN5	09RGN5 lactobacill
39	158	4.0	656	16	08K8U1	08K8U1 streptococc
40	157.5	4.0	5005	16	09P2Z5	09P2Z5 ureaplasma
41	156	4.0	1530	16	08Y479	08Y479 listeria mo
42	155	3.9	832	16	08TAF5	08TAF5 listeria mo
43	155	3.9	957	2	09AHL1	09AHL1 borrelia bu
44	153	3.9	993	5	081AL1	081AL1 plasmodium
45	153	3.9	1011	2	09AHL0	09AHL0 borrelia bu

RESULT 1

ID	08GRA2	PRELIMINARY;	PRT:	757 AA.
AC	08GRA2	01-MAR-2003 (Tremblrel. 23, Created)		
DT	01-MAR-2003 (Tremblrel. 23, last sequence update)			
DT	01-MAR-2003 (Tremblrel. 23, last annotation update)			
DE	Protein F-homologous protein.			
GN	PPHP			
OS	Streptococcus			
OC	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;			
OX	NCBI_TaxID-1314;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	STRAIN-291			
RT	Characterization of protein F-homologous protein of M1-type group A			
RL	Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.			
DR	EMBL: AB083107; BAC20340.1; -			
SQ	SEQUENCE 757 AA: 85142 MW: 3634146PF07BDPD CRC64;			
Query Match	99.9%;	Score 3941;	DB 2;	Length 757;
Best Local Similarity	99.9%;	Pred. No. 1.1e-209;		
Matches 756;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MKTRFNNKLTNTQRLVLSKSKRTYVLFVFLMIFLVSVMGAKVFGVLESSTPN	60	
DB	1	MKTRFNNKLTNTQRLVLSKSKRTYVLFVFLMIFLVSVMGAKVFGVLESSTPN	60	
QY	61	AINPDSSSEYRWYGYSGYRGHPYKQFVAVDLRVNLEGSYSYOVYCNLKKAPLGSD	120	
DB	61	AINPDSSSEYRWYGYSGYRGHPYKQFVAVDLRVNLEGSYSYOVYCNLKKAPLGSD	120	
QY	121	SSVKWYKKHDSISTKFEDYAMSPTGDELNOKLAAVYNGHPNANGIMGLEPLNAI	180	
DB	121	SSVKWYKKHDSISTKFEDYAMSPTGDELNOKLAAVYNGHPNANGIMGLEPLNAI	180	

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OY 181 RTQEAIVWVYSDNAPISNPDESEKRESNLTSTLSOLSLMRQALKOLLIDPNATKMPKQV 240
DB 181 RTQEAIVWVYSDNAPISNPDESEKRESNLTSTLSOLSLMRQALKOLLIDPNATKMPKQV 240
OY 241 PDFOLSTFSEEDKGRKYNKYONLSCGLVPTKPTPGDPMPQPPQOTTSVLKRYAI 300
DB 241 PDFOLSTFSEEDKGRKYNKYONLSCGLVPTKPTPGDPMPQPPQOTTSVLKRYAI 300
OY 301 GDYSKLLLEGATLQLTGDNVNSFOARVSSNDIGERIELSDGYTTLTLELNSPAGYSTAEPI 360
DB 301 GDYSKLLLEGATLQLTGDNVNSFOARVSSNDIGERIELSDGYTTLTLELNSPAGYSTAEPI 360
OY 361 TFEVVEAGKYTTIIDGQIENPKKEIYEPYSVEAYNDEEFVYLTQNTAKFYAKKNKS 420
DB 361 TFEVVEAGKYTTIIDGQIENPKKEIYEPYSVEAYNDEEFVYLTQNTAKFYAKKNKS 420
OY 421 SOVVYFENADLSPSPSEDEGKTMPDFTTGKYYTHIAGRDLFEKTYVPRDTPDTFLK 480
DB 421 SOVVYFENADLSPSPSEDEGKTMPDFTTGKYYTHIAGRDLFEKTYVPRDTPDTFLK 480
OY 481 HIKKVIKGYREKQAIEXSGLETOLRAATOLAIYFTDSAEIDKDLKDYHGFEGDMND 540
DB 481 HIKKVIKGYREKQAIEXSGLETOLRAATOLAIYFTDSAEIDKDLKDYHGFEGDMND 540
OY 541 STLAAKILVEYAODSNPPQLTDLDFIINNKKYQSLIGTQWHPEDLVDIIMEDKKEVI 600
DB 541 STLAAKILVEYAODSNPPQLTDLDFIINNKKYQSLIGTQWHPEDLVDIIMEDKKEVI 600
OY 601 PTHNLTLRKTYTGLAGDRTKDFHFEIELKNNKQELLSTQVTKDKNLEFKGKATINLK 660
DB 601 PTHNLTLRKTYTGLAGDRTKDFHFEIELKNNKQELLSTQVTKDKNLEFKGKATINLK 660
OY 661 HESLITLQGLPEGYSTLVKETDSEGYKVNVSQEVANATVSKTIGTSDTLAFENKKEPV 720
DB 661 HESLITLQGLPEGYSTLVKETDSEGYKVNVSQEVANATVSKTIGTSDTLAFENKKEPV 720
OY 721 VPQVQKINGYALIVAGISLIGTIGTIGTIRIKHD 757
DB 721 VPQVQKINGYALIVAGISLIGTIGTIGTIRIKHD 757

RESULT 2
O8RP53 PRELIMINARY: PRT: 756 AA.
AC 08RP53;
DT 01-JUN-2002 (TREMELREL. 21, Created)
DT 01-JUN-2002 (TREMELREL. 21, Last sequence update)
DT 01-JUN-2002 (TREMELREL. 21, Last annotation update)
DE Cpa.
GN CPA.12.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-A735;
RX MEDLINE-21843101; PubMed-11854196;
RA Bessen D.E., Kalla A.;
RT "Genomic localization of a T serotype locus to a recombinatorial zone
RT encoding extracellular matrix-binding proteins in Streptococcus
RT pyogenes."
RL Infect. Immun. 70:1159-1167(2002).
DR EMBL: AF447492; FAL86406.1; -.
SQ SEQUENCE 756 AA; 85698 MW; 88BDE087714EC464 CRC64;

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Query Match 52.2%; Score 2058.5; DB 2: Length 756;
Best Local Similarity 54.3%; Pred No. 1.2e-105;
Matches 404; Conservative 126; Mismatches 189; Indels 25; Gaps 10;

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OY 17 RVLSNKRFTVTLVGVLMFALVTSNAGTAVG---LVESSTPNAINPDSSEYRW 72
DB 14 RVSNKRKQTLVTLVGVLMFALVTSNAGTAVG---LVESSTPNAINPDSSEYRW 72

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Med Aug 20 11:56:16

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OY 73 YGESYVRGHPYKQFRAVHDLRVNLGESSRYOVYCFNLKKAFLPGSDSVYKWKYKHDG 132
DB 72 YGDSYDSHPYKQFRAVHDLRVNLGESSRYOVYCFNLKKAFLPGSDSVYKWKYKHDG 131
OY 133 ISTKEDYAMSFRITGDELNOKLRAVMTNGHPONANGIMEGLEPINALIRVQEAIVWVYSD 192
DB 132 TGDVFTNVAQPTKINGESILNNKLSTIMYNAVKNANGYMDKIEPLNALILVQEAIVWVYSD 191
OY 193 NAPISNPDESEKRESNLTSTLSOLSLMRQALKOLLIDPNATKMPKQVDDPQSTFSE 252
DB 192 SS-YGNITTLWASELKDGLIDPEQVTKMREAVSKLISDLEETSKNKLPQSGSKLNTFVPO 250
OY 253 DKGDYKNGYONLSCGLVPTKPTPGDPMPQPPQOTTSVLKRYAIGDYSKLLLEGATL 312
DB 251 D-----KSVNLSAEVYEPSPAPGSPPPQOTTSVILIRKAGDYSKLLLEGATL 304
OY 313 QLTGDNVNSFOARVSSNDIGERIELSDGYTTLTLELNSPAGYSTAEPIITFEVVEAGKYTTI 372
DB 305 RLTEGDIIDFQEKVYFQSNGTGEKIELSNGTYTLETSSPDGYKIAEPIKFRVYKKNKVEIV 364
OY 373 -IDGQIENPKKEIYEPYSVEAYNDEEFVYLTQNTAKFYAKKNKSQOVYVCEN 428
DB 365 OKDSQVBNPKKEIYEPYSVEAYNDEEFVYLTQNTAKFYAKKNKSQOVYVCEN 424
OY 429 ADLSPSPSEDEGKTMPDFTTGKYYTHIAGRDLFEKTYVPRDTPDTFLKHIKKVIE 487
DB 425 ADLSPSPSEDEGKTMPDFTTGKYYTHIAGRDLFEKTYVPRDTPDTFLKHIKKVIE 484
OY 488 KGYRKQAIEXSGLETOLRAATOLAIYFTDSAEIDKDLKDYHGFEGDMNDSTL 543
DB 485 KGYRKQAIEXSGLETOLRAATOLAIYFTDSAEIDKDLKDYHGFEGDMNDSTL 542
OY 544 AVAKILVEYAODSNPPQLTDLDFIINNKKYQSLIGTQWHPEDLVDIIMEDKKEVI 602
DB 543 AVAKILVEYAODSNPPQLTDLDFIINNKKYQSLIGTQWHPEDLVDIIMEDKKEVI 602
OY 603 THNLTLRKTYTGLAGDRTKDFHFEIELKNNKQELLSTQVTKDKNLEFKGKATINLK 662
DB 603 THNLTLRKTYTGLAGDRTKDFHFEIELKNNKQELLSTQVTKDKNLEFKGKATINLK 662
OY 663 ESLLITLQGLPEGYSTLVKETDSEGYKVNVSQEVANATVSKTIGTSDTLAFENKKEPV 722
DB 663 ESLLITLQGLPEGYSTLVKETDSEGYKVNVSQEVANATVSKTIGTSDTLAFENKKEPV 722
OY 723 TGVDQKINGYALIVAGISLIGTIGTIGTIRIKHD 757
DB 723 TGVDQKINGYALIVAGISLIGTIGTIGTIRIKHD 757

RESULT 3
O9ZB47 PRELIMINARY: PRT: 742 AA.
AC 09ZB47;
DT 01-MAY-1999 (TREMELREL. 10, Created)
DT 01-MAY-1999 (TREMELREL. 10, Last sequence update)
DT 01-DEC-2001 (TREMELREL. 19, Last annotation update)
DE Cpa.
GN CPA.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CS101;
RX Poddelski A., Moischnik M., Leonard B.A.B., Schmidt K.H.;
RA "Characterization of nra, a global negative regulator gene in group A
RT streptococci."
RL Mol. Microbiol. 31:0-0(1999).
DR EMBL: U49397; AAC97148.1; -.
SQ SEQUENCE 742 AA; 83683 MW; 97A1FF44B4ECB944 CRC64;

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